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IMPACT OF SELECTIVE LOGGING ON MATING SYSTEM AND GENE FLOW OF A TROPICAL RAIN FOREST SPECIES.

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Introduction

Conservation of genetic variability of tropical trees is an important aspect in sustainable management of forest. In tropical rain forests, most silvicultural pratices are based upon selective logging which alters genetic and demographic processes such as loss of genetic variability for adaptative evolution, random fixation of deleterious mutations or alleles by genetic drift, and inbreeding depression (Alvarez-Buylla *et al*. 1996; Barrett and Kohn 1991). Selective logging consists of removing mature trees leading to changes in the density and the spatial distribution of the reproductive trees, and the mating system. Consequently, the composition of the male and female pools, self-crossing rates and gene flow could be perturbed (Konuma *et al*., 2000; White *et al*., 2002). We assume that pollination occurs mainly between proximal trees. Our hypotheses are that logging, by reducing the density of effective reproductive trees, may modify the selfing rate as well as the average pollination distance and the genetic drift. We tested those hypotheses in the African mahogany, Sapelli (*Entandrophragma cylindricum* (Sprague) Sprague, Meliaceae) using four microsatellite nuclear markers.

Methodology

We analysed two samples of seeds from the same stand located in a Cameroonian rain forest that were collected before (2002) and after (2003) logging activities (see table 1 for details). For each sample, an average of 15-20 mother trees and 10-25 seeds per mother were collected. We characterized the mating system and gene flow before and after logging by reconstructing parental links with paternity tests using the software FaMoz (Gerber *et al*., 2003), assumed that all the trees (potential fathers) inside the stand were mapped and genotyped with four discriminate microsatellites.

Results and Discussion

Characterisation of mating system and mean pollination distances inside the stand are recorded in Table 1. We divided the total gene flow into two different components: gene flow from inside the stand when it was possible to identify the father tree inside the stand and gene flow from outside the stand in the other cases. On average, the level of gene flow received from inside the stand amounted to 31% in 2002 and to 23% in 2003. 78 trees participated as pollen donors in 2002 and 87 in 2003.

Table 1 : Characterisation of the mating system and gene flow

	No. of mother trees / total no. of trees	No. of analysed seeds	Gene flow inside the stand / No. identified fathers	average diameter of father trees inside the stand	self - fertilisation rate	Mean pollination distance inside the stand
Before logging	15/152	255	31%/78	88 cm dbh	3.1%	326 m
After logging	20/113	373	23%/87	80 cm dbh	1.6%	287 m

The rate of self-fertilisation was low even after logging and the average distance of pollination inside the stand decreased. The number of identified male parents increased in the distance class from >0 to 50m (Figure 1).

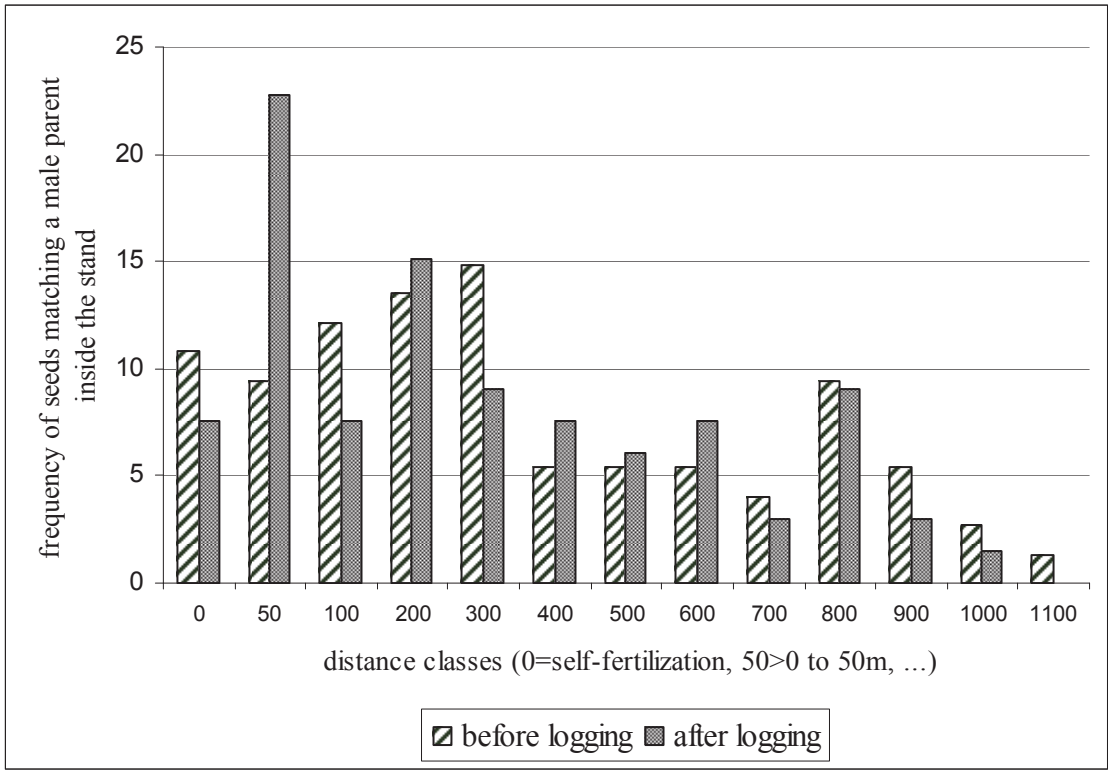

Figure 1: Distributions of identified male parents in function of distance classes inside the stand.

The geographic distribution of pollen donors are presented for 15 maternal trees before logging and for 20 maternal trees after logging (Figure 2).

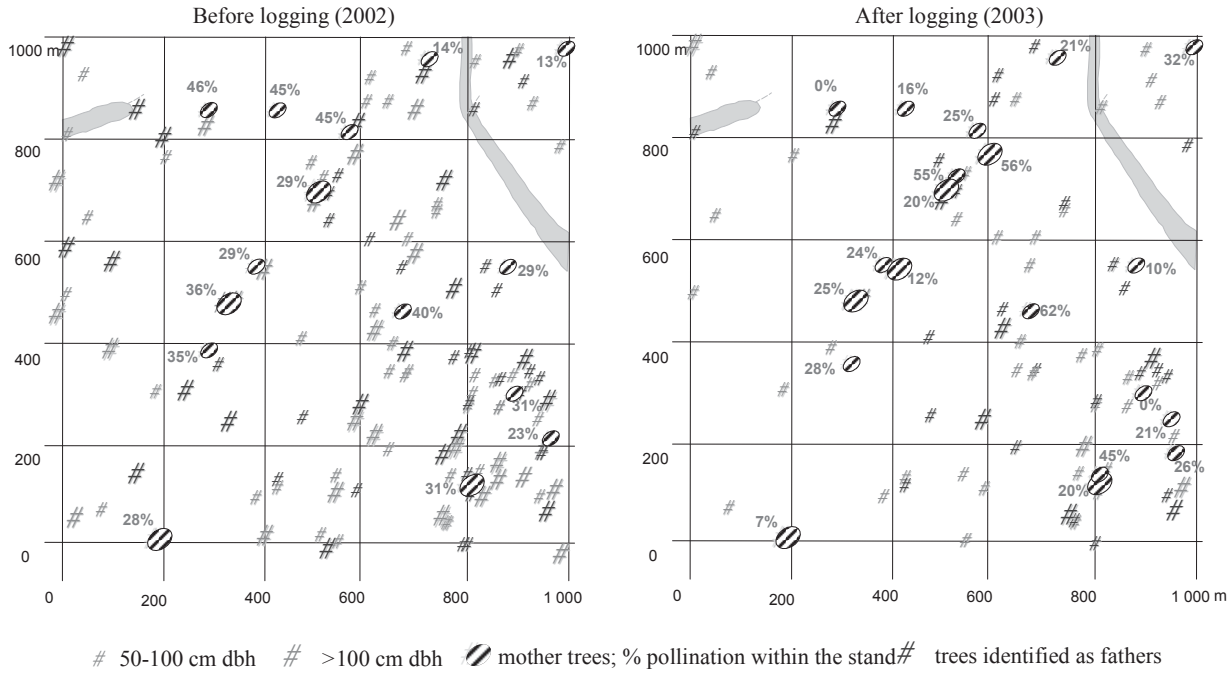

Figure 2: Map of the study stand before (2002) and after logging (2003). The locations of the trees sampled for paternity analysis and trees identified as fathers are given.

We found that gene flow coming from outside the stand varied from 54% to 87% before logging and from 38% to 100% after logging. This result is depending on the mother but it seems to be independent of the geographical location of the mother tree in the stand

Microsatellite markers appeared to be powerful tools for tracing pollen flow in a Cameroonian forest stand before and after selective logging for Sapelli, and thus to define recommendations for *in situ* conservation of the species. According to Kitamura et al. (1994) and Wickneswari et al. (2000) results show that overall outcrossing rate was high and that logging has no clear impact on the amount of selfing. We found also that selective logging increases gene flow from outside the stand indicating that pollen can move over long distances, maybe due to a an adaptative behavior of the pollinator (White et al., 2002). We need further studies on the reproduction biology of Sapelli and especially on its pollinators in order to better understand the impact of logging on gene flow. In conclusion, our results show that a single logging event in a Cameroonian forest did not cause severe changes in the genetic diversity (Lourmas et al., submitted) and in the mating system of Sapelli. Thus, selective logging seems to be a suitable strategy to ensure the sustainable use of Sapelli.

References

Alvarez-Buylla ER, Garcia-Barrios R, Lara-Moreno C, and Martinez-Ramos M.1996. *Annu Rev Ecol Sys* 27**:**387-421.

Barrett SCH and Kohn JR. 1991. *In* 'Genetics and conservation of rare plants'. (Eds DA Falk and KF Holsinger):3-30.

Gerber S, Chabrier P and Kremer A. 2003. *Mol Ecol Notes* 3**:**479-481.

Kitamura K, Mohamad Y, Ochiai O and Yoshimura H. 1994. *Pl Sp Biol*.9: 37-41.

Konuma A, Tsumura Y, Lee CT, Lee SL and Okuda T. 2000. *Mol Ecol* 9:1843-1852.

Lourmas M, Garcia F, Joly HI, and Chevallier MH. *Mol Ecol (submitted)*

White GM, Boshier DH and Powell W. 2002. *P Natl Acad Sc USA* 99**:**2038-2042.

Wickneswari R, Lee CT, Norwati M, and Boyle TJB. *In* Forest genetics and sustainability (Mathyas C ed): 171-181.